Abstract

Described is a method for identifying and quantifying of tumour-associated peptides, wherein first at least two different sources for obtaining the peptide are provided (tumourous and healthy tissue), and, separately of one another, the peptides from the different sources are chemically modified in an identical manner by using at least two different stable isotopes of the same element. Subsequently, the peptides are isolated by a chromatographic method, and the amino acid sequences of the peptides are determined, wherein the determination of the relative amount ratios of peptides having the identical sequence from different samples one to the other occurs by using a stable isotope in the chemical modification. Furthermore, the invention relates to a tumour-associated peptide having an amino acid sequence that is selected from the group consisting of SEQ-ID No. 1 to 36 from the accompanying sequence protocol, wherein the peptide has the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I. Furthermore, the invention relates to the use of the peptides for producing a medicament and for the treatment of tumourous diseases and/or adenomatous diseases. Furthermore, a pharmaceutical composition is described that comprises at least one of the peptides.